Amendments to the Specification

Please insert the following new paragraph at page 3, after line 18 (Brief Description of the Figures) as the first paragraph under the Brief Description of Figures heading.

The patent application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request of payment of the necessary fee.

Please replace the paragraph beginning at page 12, line 7, with the following rewritten paragraph:

Similar to the Stanford protocol, a cell line pool of 13 cell lines derived from different tissue origins was used as reference for all microarray hybridizations (details are available at MIAMExpress ([[http://]]www.ebi.ac.uk/miamexpress/). Probes of the cell line pool were always labeled with Cy5.

Please replace the paragraph beginning at page 12, line 24, with the following rewritten paragraph:

Microarray slides were manufactured at the Central Microarray Facility at the Netherlands Cancer Institute (Weige, et al., 2003, *Proc. Natl. Acad. Sci. U.S.A.,* 100:15901-5). Sequence-verified clones obtained from Research Genetics (Huntsville, AL) were spotted with a complexity of 19,200 spots per glass slide using the Microgrid II arrayer (Biorobotic, Cambridge, U.K.) The gene ID list can be found at [[http://]]microarrays.nki.nl. Labeled cDNA probes were heated at 95^0C for 2 minutes and added to preheated hybridization buffer (Slide hybridization buffer 1, Ambion). The probe mixture was hybridized to cDNA microarrays for 16 hours at 45^0C.

Please replace the paragraph beginning at page 13, line 3, with the following rewritten paragraph:

Fluorescent images of microarrays were obtained by using the GeneTAC™ LS II microarray scanner (Genomic Solutions; Perkin Elmer). IMAGENE v5.5 (Biodiscovery, Marina Del Rey, CA) was used to quantify and correct Cy3 and Cy5 intensities for background noise. Spot quality was assessed with the flagging tool of IMAGENE, in this study set at R>2 for both Cy3 and Cy5. Fluorescent intensities of each microarray were normalized per subgrid using the NKI MicroArray Normalization Tools ([[http://]]dexter.nki.nl) to adjust for a variety of biases that affect intensity measurements (e.g. color-, print tips, local background bias) (Yang, et al., 2002, *Nucleic Acids Res.*, 30:e15). All ratios were log2 transformed.

Please replace the paragraph beginning at page 13, line 13, with the following rewritten paragraph:

Microarray data analyses were performed with the software packages BRB Array Tools, developed by the Biometric Research Branch of the US National Cancer Institute, ([[http://]]linus.nci.nih.gov/BRB-ArrayTools.html), and Spotfire (www.spotfire.com, Goteborg, Sweden and Sommerville, MA). BRB was implemented for statistical analysis of microarray data whereas Spotfire was used for cluster analysis. The class comparison tool in BRB combines a univariate F-test and permutation test (n=2000) in order to find discriminating genes and to confirm their statistical significance. In the class comparison a significance level of 0.05 was chosen in order to limit the number of false negatives.